

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539,213
Source: PCT/10
Date Processed by STIC: 6/24/05

ENTERED



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/539,213

DATE: 06/24/2005
TIME: 15:21:15

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06242005\J539213.raw

3 <110> APPLICANT: Agrinomics LLC
 5 <120> TITLE OF INVENTION: GENERATION OF PLANTS WITH ALTERED OIL CONTENT
 7 <130> FILE REFERENCE: 6616-71292-08
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,213
 C--> 9 <141> CURRENT FILING DATE: 2005-06-17
 9 <150> PRIOR APPLICATION NUMBER: PCT/US2003/041146
 10 <151> PRIOR FILING DATE: 2003-12-18
 12 <150> PRIOR APPLICATION NUMBER: 60/434,763
 13 <151> PRIOR FILING DATE: 2002-12-18
 15 <160> NUMBER OF SEQ ID NOS: 6
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 5034
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Arabidopsis thaliana
 24 <400> SEQUENCE: 1
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 29 catgttcctc gagagtttc ttctcgttt ggatctggag acttccgcag accttcttca 180
 31 ttaaacacagc tcttaagatt gataggaagt gaattgtat ggttacttt caaaggagca 240
 33 atttttaata ctcagggtgg accgcaccag ttgtggagg agactagtc tggatcacaca 300
 35 tcttcgcgt ccagtgcgg aatgttttat aattataggc catcagcatc gcgtggagac 360
 37 tggagatata ccaggaattt cagggatgtat agagttctg taagccaaa ggaatggaaa 420
 39 tgcaatacat gggagatgag caacggatct tctagaagtt ttgagaggcc atttgttatt 480
 41 agaaatggtc ggaggtcagt ttagtgcattt ccgcataatc ttgcataatc tcattctacc 540
 43 gtggtaact ctgtttgtcc accaaactcg gctcattatc tggacaatgc gatcgttacc 600
 45 ccagttacggc ctcttaaat taaaaatggat cataaattttt cagatcaatgc gttatcactt 660
 47 ctttcagatc ctcattctgc atgttattttt ttgtttgtcc ggccttcttc tgagaacaat 720
 49 tatggcaata aggtttgttc accagcaatgc caatgcattt atttgtatgc tggcgttgc 780
 51 ttagttatgt ataattttt cttttttttt agatgtccca atccccatgc cagatgttgc ggggacttgg 840
 53 gaacaacttc gcctgaaaaga cccgcaatgc aacaatgtt tacatgttgc caatgtatgc 900
 55 gacgggtata gggaaatgtgc aaaggagatgc tctctggag caactggaa actttccatgc 960
 57 tggaaatgtt ctgggatgtt tgcatttttgc agttcaggatgc ttgttgcattt aatgttgc 1020
 59 aaaagcttgg gggcttttgc ttccatgcgtt cggaaatgc aggttcttgc taaaattttt 1080
 61 actgtgactc aatcttttc agggatgtatgc actgcgttgc ccacaaatgc tcatttttgc 1140
 63 gaggagatgtatgc ttttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 1200
 65 gagaaaaaaaaaga aatgttgcgtt taacccaaatgc gaaatgttgc caacatttttgc gggaaacggcgtt 1260
 67 ttagagggatgc tacatttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 1320
 69 gttccatgcattt atgggttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 1380
 71 tttgttgcgtt aatcatctcc gaaaggctgtatgc atagctgtatgc ttttttttttgc ttttttttttgc 1440
 73 ctttcgcctt,gtcccgttgc tagtatttttttttgc ttttttttttgc ttttttttttgc ttttttttttgc 1500
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81	aacaaacata	ggacactaaa	gcttgaaggt	agaagacact	ctcggttgt	tggaccgcgt	1740
83	tcatactgtt	gtgatggaga	tgcaaattgt	cccaaggagc	aggcttcttgc	tagtttggat	1800
85	cctaaggcaa	cagcttcttc	ttagctaaa	acactggta	gagctcctgt	gcattcaggct	1860
87	ggttagcca	aggttcctgc	tgatgtttt	gaagatagtc	ctggggaaat	taaacctcta	1920
89	tcccaatctt	ttgccactgt	tgaaagagag	gaagatatac	tgcccatacc	atctatgaag	1980
91	gcaagtgtt	cttcgaaaga	gattaacaca	cctgcttttgc	ccaatcagga	aactatttgc	2040
93	gttcttctg	ctgatgacag	catggcctcc	aaagaagact	tgttctgggc	taagtttata	2100
95	tctgccaata	agaaatatgc	ttgtgaatca	tctggagat	tcaatcaatt	gcttccaaga	2160
97	gattttaatt	cgtctgacaa	ctcaagattc	cctggcatat	gtcaaacgc	gtttgattct	2220
99	catgtccaag	aaaaatttgc	agatagggt	ggcctattga	gagctaggga	gaaaatttta	2280
101	ctcccttcagt	ttaaagcg	ttagctctca	tggaaagaaag	atttggatca	gctagcttta	2340
103	gcaaaagtacc	aatcaaagtc	tagcaaaaaaa	acagaactat	atccgaatgc	aaaaaatgg	2400
105	ggttatctga	agcttccccca	atctgtacgc	ctgaggttct	cttcttcagc	tccaaagaagg	2460
107	gatagtgttag	tccccacaac	agagctcgta	agttatatgg	aaaagctact	tccgggtacc	2520
109	catctaaagc	cttttagaga	cattttgaaa	atgcctgta	tgattttgg	tgagaaagag	2580
111	agggtgtatgt	cgaggtttat	ttcttagcaat	ggactgatttgc	aagatccatg	tgacgtttag	2640
113	aaggaaagaa	caatgattaa	tccttggacc	tcagaggaga	aagaaatctt	tctgaatttgc	2700
115	ctagcaatgc	atggaaagg	tttcaagaag	attgttcat	ctcttacca	aaagacaact	2760
117	gcccactgt	ttgattacta	ctacaaaaac	cacaagtctg	attgttttgc	gaaaataaaag	2820
119	aagcagcgt	tttatggtaa	gaaagggaaag	cacacctaca	tgttggctcc	acgaaaaaaag	2880
121	tgaaaacgt	agatggggc	tgcctctt	gatattttgc	gggatgtctc	cattatagca	2940
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127	agttttgatt	tcccacgtaa	gagaactgt	ggtgcagat	ttttagctgt	tggcctttg	3120
129	tcaccagagc	agataaaattc	ttgcttaagg	acttctgt	gctctagaga	gaggtgtat	3180
131	gatcatctga	agtttaatca	tgtcgtaaag	aaacctcg	tatctcata	tctacataat	3240
133	gagaacagca	atactctaca	caatgagaac	agcaacgaag	aatgtact	atgttcggaa	3300
135	gagagctgt	gggaaacagg	tccttattcac	tggacagat	atgagagatc	tgccttata	3360
137	cagggttttgc	cgcttttgc	caagaatttgc	gcttcataat	caaggtacgt	cgggacaaga	3420
139	tctccagatc	agtgttaagg	tttcttcagc	aaagttcg	aatgtcttgc	gttggatct	3480
141	ataaagtttgc	gatctggaaa	tgttaacaca	tccgttaatgt	ttgataatgg	caatgagggt	3540
143	ggtgggagcg	acttggaaaga	tccttgcct	atggagat	actctggcat	agtatataat	3600
145	ggagtttgc	ccaagatgg	tatgttattc	cctacccat	cttttataat	gaatcaggat	3660
147	ggtgttaatc	aatcaggctc	tgccaaatgt	aaagccgacc	tttagtagatc	agaagaagag	3720
149	aatgggcaga	aatatttgc	tctgaaatgt	gataataatc	tcgtgaacaa	tgcataatgt	3780
151	aatggcggtt	tcccagatc	agtttgc	tcttgc	atttgc	tattaatact	3840
153	gttgagagcc	agtctcagg	tgccggaaa	agcaagagca	atgtatct	gtcaatggaa	3900
155	atcgatgaag	gtgtcttac	atctgtact	atatcttgc	agccattgt	tgtggccta	3960
157	agtgttcttgc	ccaatgtt	tgtggaaacc	cctacagaaa	tctcacgaaa	gggctcagg	4020
159	gatcaagggt	ctacaatgc	taaatttgc	tcaaaatgc	aatgtggat	gtatgtat	4080
161	gcaaaacagaa	ccagaaattc	ttgccttgc	cctgaaatgt	cacccat	tttcaggat	4140
163	cctgagtg	ttcaccatgt	tccgattgt	gtgtgtacgg	aaaaccctat	aggcgtcagt	4200
165	gcaccacgag	gaaatccaaa	ttgcccata	gatggcgt	caggaaattc	tcttgcgttgc	4260
167	caagttgac	aaacacatgc	tttgggttgc	cccaagaaca	atctggat	ggatgggagg	4320
169	cttcagg	ttttagccatgt	aaaccctgt	cagattgt	tactaaatgc	gaccaataca	4380
171	gaatcttgc	aaaatccccca	gagatcagtc	acccaaatgc	tgacgttgc	aagtagatca	4440
173	aaatctgtt	tgtatgtaaa	aaaccaacgt	acaggtgt	gcttctact	caccaatgt	4500
175	actagttcag	ctccataagcc	tctggcgt	tccataaaag	agggcagatc	tggcata	4560

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177	aggagccatt	cgtttagttt	gtctgatact	gagagactcc	acaagaatgg	agatgtgaaa	4620
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181	ggaattgtca	ggtcatcatc	aaccttgagc	agggaccatg	atacaagaca	tcattacatt	4740
183	aatcagcaac	accttcagaa	cgttcccatt	acgagctacg	gtttttggga	tggcaacaga	4800
185	attcaaaccg	ggctcacatc	tttgcagag	tcggccaagt	tgcttgcag	ttgccctgaa	4860
187	gcattttcca	cgcacatctaaa	gcagcaagtt	gtaacagca	aagagattct	ggtggatgtt	4920
189	aatggtggaa	ttttgagctt	tggtaagcat	aacgaagata	gagctgagtc	ctcaagcgct	4980
191	aaggatgaag	gtaacatagg	aggggtaaat	ggtgtacag	aggcagccac	gtga	5034
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197	<213>	ORGANISM:	Arabidopsis thaliana				
199	<400>	SEQUENCE:	2				
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206	20	25	30				
209	Trp Arg Asp Ser Pro Ser Ser His His Val Pro Arg Glu Phe Ser Ser						
210	35	40	45				
213	Arg Leu Gly Ser Gly Asp Phe Arg Arg Pro Ser Ser Leu Thr Gln Leu						
214	50	55	60				
217	Leu Arg Leu Ile Gly Ser Glu Leu Met Arg Leu Leu Phe Lys Gly Ala						
218	65	70	75	80			
221	Ile Phe Asn Thr Gln Gly Gly Arg His Gln Phe Val Glu Glu Thr Ser						
222	85	90	95				
225	His Gly Tyr Thr Ser Ser Arg Ser Ser Ala Arg Met Phe Asp Asn Tyr						
226	100	105	110				
229	Arg Pro Ser Ala Ser Arg Gly Asp Trp Arg Tyr Thr Arg Asn Cys Arg						
230	115	120	125				
233	Asp Asp Arg Val Ser Val Ser Gln Lys Glu Trp Lys Cys Asn Thr Trp						
234	130	135	140				
237	Glu Met Ser Asn Gly Ser Ser Arg Ser Phe Glu Arg Pro Phe Gly Ile						
238	145	150	155	160			
241	Arg Asn Gly Arg Arg Ser Val Asp Glu Arg Pro Leu His Ala Ser Asp						
242	165	170	175				
245	Thr His Ser Thr Val Val Asn Ser Leu Asp Pro Ala Asn Ser Ala His						
246	180	185	190				
249	Tyr Leu Asp Asn Glu Ile Ser Thr Pro Val Arg Ser Leu Lys Ile Lys						
250	195	200	205				
253	Asn Glu His Lys Phe Ser Asp Gln Arg Leu Ser Leu Pro Ser Asp Pro						
254	210	215	220				
257	His Ser Glu Cys Ile Ser Leu Phe Glu Arg Pro Ser Ser Glu Asn Asn						
258	225	230	235	240			
261	Tyr Gly Asn Lys Val Cys Ser Pro Ala Lys Gln Cys Asn Asp Leu Met						
262	245	250	255				
265	Tyr Gly Arg Arg Leu Val Ser Asp Asn Ser Leu Asp Ala Pro Ile Pro						
266	260	265	270				
269	Asn Ala Glu Leu Glu Gly Thr Trp Glu Gln Leu Arg Leu Lys Asp Pro						
270	275	280	285				

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273 Gln Asp Asn Asn Ser Leu His Gly Ile Asn Asp Ile Asp Gly Asp Arg
274 290 295 300
277 Lys Cys Ala Lys Glu Ser Ser Leu Gly Ala Thr Gly Lys Leu Pro Leu
278 305 310 315 320
281 Trp Asn Ser Ser Gly Ser Phe Ala Ser Gln Ser Ser Gly Phe Ser His
282 325 330 335
285 Ser Ser Ser Leu Lys Ser Leu Gly Ala Val Asp Ser Ser Asp Arg Lys
286 340 345 350
289 Ile Glu Val Leu Pro Lys Ile Val Thr Val Thr Gln Ser Ser Ser Gly
290 355 360 365
293 Asp Ala Thr Ala Cys Ala Thr Thr His Leu Ser Glu Glu Met Ser
294 370 375 380
297 Ser Arg Lys Lys Gln Arg Leu Gly Trp Gly Glu Gly Leu Ala Lys Tyr
298 385 390 395 400
301 Glu Lys Lys Lys Val Asp Val Asn Pro Asn Glu Asp Gly Thr Thr Leu
302 405 410 415
305 Met Glu Asn Gly Leu Glu Glu Leu His Ser Leu Asn Lys Asn Ile Ala
306 420 425 430
309 Asp Lys Ser Pro Thr Ala Ala Ile Val Pro Asp Tyr Gly Ser Pro Thr
310 435 440 445
313 Thr Pro Ser Ser Val Ala Cys Ser Ser Ser Pro Gly Phe Ala Asp Lys
314 450 455 460
317 Ser Ser Pro Lys Ala Ala Ile Ala Ala Ser Asp Val Ser Asn Met Cys
318 465 470 475 480
321 Arg Ser Pro Ser Pro Val Ser Ser Ile His Leu Glu Arg Phe Pro Ile
322 485 490 495
325 Asn Ile Glu Glu Leu Asp Asn Ile Ser Met Glu Arg Phe Gly Cys Leu
326 500 505 510
329 Leu Asn Glu Leu Leu Gly Thr Asp Asp Ser Gly Thr Gly Asp Ser Ser
330 515 520 525
333 Ser Val Gln Leu Thr Ser Met Asn Thr Leu Leu Ala Trp Lys Gly Glu
334 530 535 540
337 Ile Leu Lys Ala Val Glu Met Thr Glu Ser Glu Ile Asp Leu Leu Glu
338 545 550 555 560
341 Asn Lys His Arg Thr Leu Lys Leu Glu Gly Arg Arg His Ser Arg Val
342 565 570 575
345 Val Gly Pro Ser Ser Tyr Cys Cys Asp Gly Asp Ala Asn Val Pro Lys
346 580 585 590
349 Glu Gln Ala Ser Cys Ser Leu Asp Pro Lys Ala Thr Ala Ser Ser Val
350 595 600 605
353 Ala Lys Thr Leu Val Arg Ala Pro Val His Gln Ala Gly Leu Ala Lys
354 610 615 620
357 Val Pro Ala Asp Val Phe Glu Asp Ser Pro Gly Glu Val Lys Pro Leu
358 625 630 635 640
361 Ser Gln Ser Phe Ala Thr Val Glu Arg Glu Glu Asp Ile Leu Pro Ile
362 645 650 655
365 Pro Ser Met Lys Ala Ala Val Ser Ser Lys Glu Ile Asn Thr Pro Ala
366 660 665 670
369 Phe Ala Asn Gln Glu Thr Ile Glu Val Ser Ser Ala Asp Asp Ser Met

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370	675	680	685
373	Ala Ser Lys Glu Asp Leu Phe Trp Ala Lys Leu Leu Ser Ala Asn Lys		
374	690	695	700
377	Lys Tyr Ala Cys Glu Ser Ser Gly Val Phe Asn Gln Leu Leu Pro Arg		
378	705	710	715
381	Asp Phe Asn Ser Ser Asp Asn Ser Arg Phe Pro Gly Ile Cys Gln Thr		
382	725	730	735
385	Gln Phe Asp Ser His Val Gln Glu Lys Ile Ala Asp Arg Val Gly Leu		
386	740	745	750
389	Leu Arg Ala Arg Glu Lys Ile Leu Leu Gln Phe Lys Ala Phe Gln		
390	755	760	765
393	Leu Ser Trp Lys Lys Asp Leu Asp Gln Leu Ala Leu Ala Lys Tyr Gln		
394	770	775	780
397	Ser Lys Ser Ser Lys Lys Thr Glu Leu Tyr Pro Asn Ala Lys Asn Gly		
398	785	790	795
401	Gly Tyr Leu Lys Leu Pro Gln Ser Val Arg Leu Arg Phe Ser Ser Ser		
402	805	810	815
405	Ala Pro Arg Arg Asp Ser Val Val Pro Thr Thr Glu Leu Val Ser Tyr		
406	820	825	830
409	Met Glu Lys Leu Leu Pro Gly Thr His Leu Lys Pro Phe Arg Asp Ile		
410	835	840	845
413	Leu Lys Met Pro Ala Met Ile Leu Asp Glu Lys Glu Arg Val Met Ser		
414	850	855	860
417	Arg Phe Ile Ser Ser Asn Gly Leu Ile Glu Asp Pro Cys Asp Val Glu		
418	865	870	875
421	Lys Glu Arg Thr Met Ile Asn Pro Trp Thr Ser Glu Glu Lys Glu Ile		
422	885	890	895
425	Phe Leu Asn Leu Leu Ala Met His Gly Lys Asp Phe Lys Lys Ile Ala		
426	900	905	910
429	Ser Ser Leu Thr Gln Lys Thr Thr Ala Asp Cys Ile Asp Tyr Tyr Tyr		
430	915	920	925
433	Lys Asn His Lys Ser Asp Cys Phe Gly Lys Ile Lys Lys Gln Arg Ala		
434	930	935	940
437	Tyr Gly Lys Glu Gly Lys His Thr Tyr Met Leu Ala Pro Arg Lys Lys		
438	945	950	955
441	Trp Lys Arg Glu Met Gly Ala Ala Ser Leu Asp Ile Leu Gly Asp Val		
442	965	970	975
445	Ser Ile Ile Ala Ala Asn Ala Gly Lys Val Ala Ser Thr Arg Pro Ile		
446	980	985	990
449	Ser Ser Lys Lys Ile Thr Leu Arg Gly Cys Ser Ser Ala Asn Ser Leu		
450	995	1000	1005
453	Gln His Asp Gly Asn Asn Ser Glu Gly Cys Ser Tyr Ser Phe Asp		
454	1010	1015	1020
457	Phe Pro Arg Lys Arg Thr Ala Gly Ala Asp Val Leu Ala Val Gly		
458	1025	1030	1035
461	Pro Leu Ser Pro Glu Gln Ile Asn Ser Cys Leu Arg Thr Ser Val		
462	1040	1045	1050
465	Ser Ser Arg Glu Arg Cys Met Asp His Leu Lys Phe Asn His Val		
466	1055	1060	1065

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/24/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 661,662,663,664,665,1186

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:660

M:341 Repeated in SeqNo=5